Epps

1635

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/155,676*

DATE: 02/29/2000
TIME: 01:54:05

INPUT SET: S34879.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

ENTERED

```
1                           SEQUENCE LISTING
2
3    (1)      General Information:
4
5         (i) APPLICANT: WALLACH, David
6                        MALININ, Nikolai
7                        BOLDIN, Mark
8                        KOVALENKO, Andrei
9                        METT, Igor
10
11       (ii) TITLE OF INVENTION: MODULATORS OF TNF RECEPTOR ASSOCIATED
12            FACTOR (TRAF), THEIR PREPARATION AND USE
13
14      (iii) NUMBER OF SEQUENCES: 20
15
16       (iv) CORRESPONDENCE ADDRESS:
17            (A) ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C.
18            (B) STREET: 624 Ninth Street, N.W., Suite 300
19            (C) CITY: Washington
20            (D) STATE: D.C.
21            (E) COUNTRY: USA
22            (F) ZIP: 20001
23
24        (v) COMPUTER READABLE FORM:
25            (A) MEDIUM TYPE: Floppy disk
26            (B) COMPUTER: IBM PC compatible
27            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29
30       (vi) CURRENT APPLICATION DATA:
31            (A) APPLICATION NUMBER: US 09/155,676
32            (B) FILING DATE: 04-JAN-1999
33            (C) CLASSIFICATION:
34
35      (vii) PRIOR APPLICATION DATA:
36            (A) APPLICATION NUMBER: PCT/IL97/00117
37            (B) FILING DATE: 01-APR-1997
38
39      (vii) PRIOR APPLICATION DATA:
40            (A) APPLICATION NUMBER: IL 117800
41            (B) FILING DATE: 02-APR-1996
42
43      (vii) PRIOR APPLICATION DATA:
44            (A) APPLICATION NUMBER: IL 119133
45            (B) FILING DATE: 26-AUG-1996
46
```

INPUT SET: S34879.raw

```
47      (viii) ATTORNEY/AGENT INFORMATION:
48              (A) NAME: BROWDY, Roger L.
49              (B) REGISTRATION NUMBER: 25,618
50              (C) REFERENCE/DOCKET NUMBER: WALLACH=21
51
52       (ix) TELECOMMUNICATION INFORMATION:
53              (A) TELEPHONE: 202-628-5197
54              (B) TELEFAX: 202-737-3528
55
56
57   (2) INFORMATION FOR SEQ ID NO: 1:
58
59        (i) SEQUENCE CHARACTERISTICS:
60              (A) LENGTH: 1906 base pairs
61              (B) TYPE: nucleic acid
62              (C) STRANDEDNESS: single
63              (D) TOPOLOGY: linear
64
65       (ii) MOLECULE TYPE: cDNA
66
67       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
68
69   CATTGGGTCA CGCGGTGGCG GCGCTCTAGA ATAGTGGATC CCCCGGGCTG CAGGAATTCG      60
70
71   ATTCGAGGCC ACGAAGGCCG GCGGCGCGGC GCANGCACCG GCCCGGGGAN AGGCNCCATG     120
72
73   AGCGGATCNC NGAACNATGA CAAAAGACAA TTTCTGCTGG AGCGACTGCT GGATGCAGTG     180
74
75   AAACAGTGCC AGATCCGCTT TNGAGGGAGA AAGGAGATTG CCTCGGATTC CGACAGCAGG     240
76
77   GTCACCTGTC TGTGTGCCCA GTTTGAAGCC GTCCTGCAGC ATGGCTTGAA GAGGAGTCGA     300
78
79   GGATTGGCAC TCACAGCGGC AGCGATCAAG CAGGCAGCGG GCTTTGCCAG CAAAACCGAA     360
80
81   ACAGAGCCCG TGTTCTGGTA CTACGTGAAG GAGGTCCTCA ACAAGCACGA GCTGCAGCGC     420
82
83   TTCTACTCCC TGCGCCACAT CGCCTCAGAC GTGGGCCGGG GTCGCGCCTG GCTGCGCTGT     480
84
85   GCCCTCAACG AACACTCCCT GGAGCGCTAC CTGCACATGC TCCTGGCCGA CCGCTGCAGG     540
86
87   CTGAGCACTT TTTATGAAGA CTGGTCTTTT GTGATGGATG AAGAAAGGTC CAGTATGCTT     600
88
89   CCTACCATGG CAGCAGGTCT GAACTCCATA CTCTTTGCGA TTAACATCGA CAACAAGGAT     660
90
91   TTGAACGGGC AGAGTAAGTT TGCTCCCACC GTTTCAGACC TCTTAAAGGA GTCAACGCAG     720
92
93   AACGTGACCT CCTTGCTGAA GGAGTCCACG CAAGGAGTGA GCAGCCTGTT CAGGGAGATC     780
94
95   ACAGCCTCCT CTGCCGTCTC CATCCTCATC AAACCTGAAC AGGAGACCGA CCCTTGCCTG     840
96
97   TCGTGTCCAG GAATGTCAGT GCTGATGCCA AATGCAAAAA GGAGCGGAAG AAGAAAAAGA     900
98
99   AAGTGACCAA CATAATCTCA TTTGATGATG AGGAAGATGA GCAGAACTCT GGGGACGTGT     960
```

INPUT SET: S34879.raw

```
100
101   TTAAAAAGAC ACCTGGGGCA GGGGAGAGCT CAGAGGACAA CTCCGACCGC TCCTCTGTCA   1020
102
103   ATATCATGTC CGCCTTTGAA AGCCCCTTCG GGCCTAACTC CAATGGAATC AGAGCAGCAA   1080
104
105   CTCATGGAAA ATTGATTCCC TGTCTTTGAA CGGGGAGTTT GGGTACCAGA AGCTTGATGT   1140
106
107   GAAAAGCATC GATGATGAAG ATGTGGATGA AAACGAAGAT GACGTGTATG GAAACTCATC   1200
108
109   AGGAAGGAAG CACAGGGGCC ACTCGGAGTC GCCCGAGAAG CCACTGGAAG GAACACCTG   1260
110
111   CCTCTCCCAG ATGCACAGCT GGGCTCCGCT GAAGGTGCTG CACAATGACT CCGACATCCT   1320
112
113   CTTCCCTGTC AGTGGCGTGG GCTCCTACAG CCCAGCAGAT GCCCCCCTCG GAAGCCTGGA   1380
114
115   GAACGGGACA GGACCAGAGG ACCACGTTCT CCCGGATCCT GGACTTCGGT ACAGTGTGGA   1440
116
117   AGCCAGCTCT CCAGGCCACG GAAGTCCTCT GAGCAGCCTG TTACTTCTGC CTCAGTGCCA   1500.
118
119   GAGTCCATGA CAATTAGTGA ACTGCGCCAG GCCACTGTGG CCATGATGAA CAGGAAGGAT   1560
120
121   GAGCTGGAGG AGGAGAACAG ATCACTGCGA AACCTGCTCG ACGGTGAGAT GGAGCACTCA   1620
122
123   GCCGCGCTCC GGCAAGAGGT GGACACCTTG AAAAGGAAGG TGGCTGAACA GGAGGAGCGG   1680
124
125   CAGGGCATGA AGGTCCAGGC GCTGGCCAGC TATCTTTGCT ATTTTGTGAG GAGATTCTAA   1740
126
127   CCCCACGTGA GAACCATGTG GTGGAGAAAT GGAGGGAGAG AGAAATCCAA CAGTTCCTGA   1800
128
129   TAGTCTCATT TGAGCTCCTG GATCCAGTCT TTCCTGAAGC TGTGTTTCCT CTGGACTTTT   1860
130
131   CATGTATGTG AGCCAATAAA TTGCTTTCAT TCCTTGAAAA AAAAAA   1906
132
133   (2) INFORMATION FOR SEQ ID NO: 2:
134
135       (i) SEQUENCE CHARACTERISTICS:
136           (A) LENGTH: 604 amino acids
137           (B) TYPE: amino acid
138           (C) STRANDEDNESS: single
139           (D) TOPOLOGY: linear
140
141      (ii) MOLECULE TYPE: protein
142
143      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
144
145       Xaa Thr Gly Pro Gly Xaa Gly Xaa Met Ser Gly Ser Xaa Asn Xaa Asp
146       1               5                   10                  15
147
148       Lys Arg Gln Phe Leu Leu Glu Arg Leu Leu Asp Ala Val Lys Gln Cys
149                   20                  25                  30
150
151       Gln Ile Arg Phe Xaa Gly Arg Lys Glu Ile Ala Ser Asp Ser Asp Ser
152                   35                  40                  45
```

```
153
154   Arg Val Thr Cys Leu Cys Ala Gln Phe Glu Ala Val Leu Gln His Gly
155       50              55              60
156
157   Leu Lys Arg Ser Arg Gly Leu Ala Leu Thr Ala Ala Ala Ile Lys Gln
158   65              70              75              80
159
160   Ala Ala Gly Phe Ala Ser Lys Thr Glu Thr Glu Pro Val Phe Trp Tyr
161               85              90              95
162
163   Tyr Val Lys Glu Val Leu Asn Lys His Glu Leu Gln Arg Phe Tyr Ser
164           100             105             110
165
166   Leu Arg His Ile Ala Ser Asp Val Gly Arg Gly Arg Ala Trp Leu Arg
167           115             120             125
168
169   Cys Ala Leu Asn Glu His Ser Leu Glu Arg Tyr Leu His Met Leu Leu
170       130             135             140
171
172   Ala Asp Arg Cys Arg Leu Ser Thr Phe Tyr Glu Asp Trp Ser Phe Val
173   145             150             155             160
174
175   Met Asp Glu Glu Arg Ser Ser Met Leu Pro Thr Met Ala Ala Gly Leu
176               165             170             175
177
178   Asn Ser Ile Leu Phe Ala Ile Asn Ile Asp Asn Lys Asp Leu Asn Gly
179           180             185             190
180
181   Gln Ser Lys Phe Ala Pro Thr Val Ser Asp Leu Leu Lys Glu Ser Thr
182           195             200             205
183
184   Gln Asn Val Thr Ser Leu Leu Lys Glu Ser Thr Gln Gly Val Ser Ser
185       210             215             220
186
187   Leu Phe Arg Glu Ile Thr Ala Ser Ser Ala Val Ser Ile Leu Ile Lys
188   225             230             235             240
189
190   Pro Glu Gln Glu Thr Asp Pro Cys Leu Ser Cys Pro Gly Met Ser Val
191               245             250             255
192
193   Leu Met Pro Asn Ala Lys Arg Ser Gly Arg Arg Lys Arg Lys Xaa Pro
194               260             265             270
195
196   Thr Xaa Ser His Leu Met Met Arg Lys Met Ser Arg Thr Leu Gly Thr
197           275             280             285
198
199   Cys Leu Lys Arg His Leu Gly Gln Gly Arg Ala Gln Arg Thr Thr Pro
200       290             295             300
201
202   Thr Ala Pro Leu Ser Ile Ser Cys Pro Pro Leu Lys Ala Pro Ser Gly
203   305             310             315             320
204
205   Leu Thr Pro Met Glu Ser Glu Gln Gln Leu Met Glu Asn Xaa Phe Pro
```

INPUT SET: S34879.raw

```
206                         325                 330                 335
207
208     Val Phe Glu Arg Gly Val Trp Val Pro Glu Ala Xaa Cys Glu Lys His
209                 340                 345                 350
210
211     Arg Xaa Xaa Arg Cys Gly Xaa Lys Arg Arg Xaa Arg Val Trp Lys Leu
212                 355                 360                 365
213
214     Ile Arg Lys Glu Ala Gln Gly Pro Leu Gly Val Ala Arg Glu Ala Thr
215             370                 375                 380
216
217     Gly Arg Glu His Leu Pro Leu Pro Asp Ala Gln Leu Gly Ser Ala Glu
218     385                 390                 395                 400
219
220     Gly Ala Ala Gln Xaa Leu Arg His Pro Leu Pro Cys Gln Trp Arg Gly
221                 405                 410                 415
222
223     Leu Leu Gln Pro Ser Arg Cys Pro Pro Arg Lys Pro Gly Glu Arg Asp
224                 420                 425                 430
225
226     Arg Thr Arg Gly Pro Arg Ser Pro Gly Ser Trp Thr Ser Val Gln Cys
227             435                 440                 445
228
229     Gly Ser Gln Leu Ser Arg Pro Arg Lys Ser Ser Glu Gln Pro Val Thr
230         450                 455                 460
231
232     Ser Ala Ser Val Pro Glu Ser Met Thr Ile Ser Glu Leu Arg Gln Ala
233     465                 470                 475                 480
234
235     Thr Val Ala Met Met Asn Arg Lys Asp Glu Leu Glu Glu Glu Asn Arg
236                 485                 490                 495
237
238     Ser Leu Arg Asn Leu Leu Asp Gly Glu Met Glu His Ser Ala Ala Leu
239             500                 505                 510
240
241     Arg Gln Glu Val Asp Thr Leu Lys Arg Lys Val Ala Glu Gln Glu Glu
242             515                 520                 525
243
244     Arg Gln Gly Met Lys Val Gln Ala Leu Ala Ser Tyr Leu Cys Tyr Phe
245         530                 535                 540
246
247     Val Arg Arg Phe Xaa Pro His Val Arg Thr Met Trp Trp Arg Asn Gly
248     545                 550                 555                 560
249
250     Gly Arg Glu Lys Ser Asn Ser Ser Xaa Xaa Ser His Leu Ser Ser Trp
251                 565                 570                 575
252
253     Ile Gln Ser Phe Leu Lys Leu Cys Phe Leu Trp Thr Phe His Val Cys
254                 580                 585                 590
255
256     Glu Pro Ile Asn Cys Phe His Ser Leu Lys Lys Lys
257                 595                 600
258
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/155,676*

INPUT SET: S34879.raw

Line   Error   Original Text